

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2002, 03:41:53 ; Search time 1909.32 Seconds
(without alignments)
24735.349 Million cell updates/sec

Title: US-09-652-292-1
Perfect score: 4395
Sequence: 1 gagggggctctgccagcc.....attatttgtaaaaaaaaaa 4395

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578	13.2	678	13	AQ037826 CIT-HSP-2
2	576	13.1	580	10	AA628914 af28a03.s
3	478	10.9	479	10	AL449907 AL449907
4	477	10.9	528	10	AA404352 zv63f10.s
5	466	10.6	466	10	AL449914 AL449914
6	465	10.6	481	10	AL449906 AL449906
7	460	10.5	461	10	AL449913 AL449913
8	454	10.3	454	10	AI334230 qq09h04.x
9	449	10.2	563	10	AI042706 uc76f10.x
10	408	9.3	459	10	AL449887 AL449887
11	404	9.2	532	10	AI041537 oy82b10.x
12	384	8.7	859	11	BG563879 602584689

13	378	8.6	450	10	AL449886
14	377	8.6	475	10	AL449910
15	366	8.3	685	11	BG568246 602587156
16	364	8.3	425	10	AA134031 z134a09.r
17	364	8.3	1049	11	BF688799 602184982
18	354	8.1	456	10	AA115737 zk96b03.s
19	351	8.0	910	10	AL554162 AL554162
20	344	7.8	363	10	AL449889
21	335	7.6	706	11	BG566556 602585583
22	320	7.3	368	11	CO4258 Huma
23	310	7.1	467	10	AA403072 zv63f10.r
24	290	6.6	341	10	AL449890
25	289	6.6	925	11	BG569139 602588391
26	283	6.4	402	10	AL449905
27	283	6.4	453	10	AA133497
28	279	6.3	624	11	W02942
29	275	6.3	342	11	W31922
30	271	6.2	450	10	AI081145
31	269	6.1	495	10	AA007343
32	263	6.0	330	10	AI289525
33	260	5.9	396	10	AL449904
34	259	5.9	431	10	AI097288
35	238	5.4	358	11	W38959
36	234	5.3	372	10	AI088144
37	227	5.2	235	10	AL449622
38	219	5.0	405	10	AI753392
39	216	4.9	454	10	AI753293
40	207	4.7	318	10	AI753418
41	207	4.7	354	10	AI277131
42	207	4.7	561	10	AA133966
43	206	4.7	306	10	AA313045
44	206	4.7	523	10	AW298226
45	199	4.5	242	10	AL449623

ALIGNMENTS

RESULT 1

AQ037826

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AQ037826 678 bp DNA GSS 11-JUL-1998
CIT-HSP-2326P11.TF CIT-HSP Homo sapiens genomic clone 2326P11, DNA
sequence.
AQ037826
AQ037826.1 GI:3303658
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2326P11.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@reagen.com). BAC
end search page:
http://www.tigr.org/tdb/human/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source
1..678
/organism="Homo sapiens"

AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R., and Wilson, R.

TITLE WashU-NCI human EST Project

JOURNAL Unpublished (1997)

COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 481.

FEATURES Location/Qualifiers
source 1..580
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1032940"
/dev_stage="8-9 weeks"
/lab_host="DH10b"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - Oligo(dT) primer [5'-TGTTACCACTGAAGTCAGGAGCGGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 197 a 104 c 90 g 189 t

ORIGIN

Query Match 13.1%; Score 576; DB 10; Length 580;
Best Local Similarity 100.0%; Pred. No. 1.2e-211;
Matches 576; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3637 catcatgttagctcttggtgtctaactgctgtgggagtgcttttctatcacaaagt 3696
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Db 580 CATCATGTTAGTCTTTGGTTGCTTAACCTGGCTGGGGAGTGTGTTGATCACAAAGAT 521
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QY 3697 tagagaggactacacatcaggcttgatttattgttctgattcttagacttcagacac 3756
|||||
Db 520 TAGAGAGGACTACACATCAGGCTTGATTTATGTTGTTGATTTCTAGACTTCAGAAC 461
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QY 3757 atgctggataaattgcagtaatgcataataacttaaaagtatgcttgtttgtagcca 3816
|||||
Db 460 ATGCTGGATAAATGTTCAGTAATGCAAAATTAACCTTTAAAGTATGCTGTTGTTGAGCCA 401
|||||

QY 3817 atacatggtgtatagcaccacaaaatgagggattattcttcagtaattgaacactgc 3876
|||||
Db 400 ATACATGTTGATAGCACCCAAAATGAGGAGTATTCTTCCAGTAGTTGAACACTGTC 341
|||||

QY 3877 atccgttcagctgacagctgcataatcatttaagaaggagttctgcatttcattcca 3936
|||||
Db 340 ATCCGTTTTCCAGTGCAGAGTGTCAAAATCATTTAAGAAGGAGTCTCGACATTCATTTCA 281
|||||

QY 3937 ttgtttacttttcttccctcaactagtgtaacacaaaatttcacacaggaattcatgcgc 3996
|||||
Db 280 TTGTTTACTTTGTCTTCCCTACCTAGTGTAAACAAAAATTTCAACCAGCAGCATTCATCGCG 221
|||||

QY 3997 aacctatacccatcttcagtcgcttagctgtacaggtatcatcagggaatttttattcgtagtc 4056
|||||
Db 220 AACCTATACCCATTCTTCAGTGCCTAGCTGTACAGTATACAGGATTTTATTCTCGTAGTC 161
|||||

QY 4057 taattttgcaaatcatcgcccaaatcgcagtgatagttgcatttggatacaagggtttggc 4116
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Db 160 TAAATTTGTCAANTCATGCCAAATTCGACGTGATGATGTTGACTTTGGATACAAAGTTTGGC 101
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Qy	3065	ggcctgggaaattctacttatctcaattaccacaggtccctctctcttggaccctgtaaagg	3124
Db	118	GGCTGGGAAATTCTACTTATCTCTATTACCCAGGFCCTCTCTCTGGACCCCTGTAAAGG	59
Qy	3125	gtcagggtgatcagatgggggactgagcaagtagctatgctgcagatcatgtcaagg	3182
Db	58	GTCAAGGTGAATCAGATGGGGGACTGAGCAANGTAGCTATGACTGCAGATCATGTAAAGG	1
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LOCUS			
DEFINITION		AA040352 528 bp mRNA EST 16-MAY-1997	
ACCESSION		2v63f10.s1 Soares_total_fetus_NB2HF8_9w Homo sapiens cDNA clone	
VERSION		IMAGE:758347 3', mRNA sequence.	
KEYWORDS		AA040352	
SOURCE		AA040352.1 GI:2059077	
ORGANISM		human.	
REFERENCE		Homo sapiens	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 528)	
TITLE		Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisels,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.	
JOURNAL		WashU-Merck EST Project 1997	
COMMENT		Unpublished (1997) Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: estewatson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. Et from Amersham High quality sequence stop: 464. Location/Qualifiers 1..528 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="IMAGE:758347" /dev_stage="8-9 weeks" /lab_host="DH108" /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I - oligo(dT) primer [5' TGTTACCACTCGAAGTCGGAGCGGCTTAATTTTTTTTTTTTTTTT 3'] Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."	
FEATURES			
source		181 a 77 c 75 g 195 t	
BASE COUNT			
ORIGIN			
Query Match		10.9%; Score 477; DB 10; Length 528;	
Best Local Similarity		99.8%; Pred. No. 1.9e-173;	
Matches		527; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	3865	tgaacactgctatccgctttcagctgcagctgctcaaatcatttaagagaggttctga	3924
Db	528	TTGAACACTGCTATCCCTTTTCAGCTGACAGTGTCAATCATTTAAAGAGGAGTCTCTGA	469
Qy	3925	cattcatcttcattgttttacttttcttcctcactagtgtaacacaaattccaacca	3984
Db	468	CATTCAATTTTCATTTGTTTACTTTTGTCTTCCTCACCTAGTGTAAACAAAAAATTTCAACCA	409
Qy	3985	gcattcatgcgaacctataccattcttcagtgctcagctgtacatttccagggattt	4044

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Db 408 GCATTTCATGCCCAACCTATACCCATTCTTCAGTGCCTAGCTGATACAGTTATACGGGATTT 349
QY 4045 ttattcgtagtttaatttgcacaaatcattgcccataatgcagtgatgagttgacttggat 4104
Db 348 TTATTTCGTAGTCTAATTTTGTCAAAATCATGTCGCAAAATGCGCAGTATAGTTGACTTTGGAT 289
QY 4105 acaaggtttggcaaaaaaaataattacaataattctctgtaagaatcaattgactata 4164
Db 288 ACAAGGTTTGGCAAAAAAATAATTAACAAAATATCTGTGAAGAATCAATTTGGCTATATA 229
QY 4165 tggatttttagataaagaataattacaataaagaatatttacaataaagaagtttattatt 4224
Db 228 TGGAAATTTAGGATAAAGAATAATTTACAAATAAAGAATAATTTACAAATAAAGAGTTTATTATT 169
QY 4225 atttgaagttgtgtgcaaaaacataccctttatctctctataaatttatacacaaaaa 4284
Db 168 ATTTGTAAGTTGTGAGCAACAACATACCTTTTATCTCTGTAAATTTATACACACAAAA 109
QY 4285 attacaagaattctctgaagaatttaattggtctatatggaatttaggataagaattttac 4344
Db 108 ATTACAAAAGATTTCTGTAAGAATTAATTTGGCTATATGGAATTTAGATAGAATATTATAC 49
QY 4345 aataaagattattacataaagatttggatttattattttgtaaaaaaa 4392
Db 48 AATAAAGAGTATTACAAATAAAGAGTTTGTATTATTATTGTAATAAAAAA 1

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RESULT 5
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LOCUS AL449914 466 bp mRNA EST 15-NOV-2000
DEFINITION AL449914 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449914
VERSION AL449914.1 GI:11181539
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 466)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : scc3335.
Location/Qualifiers
1. .466
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="Lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"

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FEATURES
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117 a 149 c 141 g 59 t
BASE COUNT 117 a 149 c 141 g 59 t
ORIGIN

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Query Match 10.6%; Score 466; DB 10; Length 466;
Best Local Similarity 100.0%; Pred. No. 3 6e-169;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 309 gaccttggattatgaactgcagtcataatcagtgccctgctgccactgcagcttgact 368
Db 466 GACCTTTGGTTATGACTGGCAGTCATATCAGGTGCCCTGCTGCCACTGCAGCTTGCAT 407
QY 369 tgggctaagctgctgtgagcaggattcctctggtggcagcgtctctctggggtctctc 428

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Db 406 TGGGCTAAAGCTGCTTGGAGCAGGAGTTCTTGGTGGCAGCCTGCTCCTGGGGGCTCTCCT 347
QY 429 cgctccctggttgggtggcttctcattgaactgctatggcaggaagcaagcattcctcg 488
Db 346 CGCTCCCTGGTGGTGGCTTCCTCATTTGACTGCTATGGCAGGAAGCAATCCTCGG 287
QY 489 gagcaacttgggtgctgtgagcagcagcctgacccctggcctggcctgggttccctggcctg 548
Db 286 GAGCAACTTGGTGTCTGCTGGCAGGACCTGACCCCTGGGCGCTGGCTGGTTCCTCGGCTG 227
QY 549 gctggttccctggcctggcctggtgtgtgtgcttcccttcccttcccttcccttccctt 608
Db 226 GCTGGTCCCTGGGCGCGGCTGTGGTGGCTTCCCATTTCCCTCTCCTCCATGGCTTGGTG 167
QY 609 tatctacgtgtcagagctggttggccacgcagcagcgggagtgctggttccctctatga 668
Db 166 TATCTACGTGTGAGAGCTGTGGGGCCACGGCAGGGGAGTGTGGTGTCCCTCTATGA 107
QY 669 ggcaggaatccacgtgggaatcctgctctctctctcctcaactatgacatgacctgggtac 728
Db 106 GGCAGGCATCACCGTGGGATCCTGCTCTATGTCCTCAACTATGACATGACATGGCTGGTAC 47
QY 729 cccctgggagatgagagcaatgttggctggcctggcctggcctggcctggcctggct 774
Db 46 CCCCTGGGATGGAGGCACATGTTGGGCTGGGCGCACTGCACCTGCT 1

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RESULT 6
AL449906
LOCUS AL449906 481 bp mRNA EST 15-NOV-2000
DEFINITION AL449906 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449906
VERSION AL449906.1 GI:11181531
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 481)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : scc3096.
Location/Qualifiers
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/map="20"
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technique"

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BASE COUNT 114 a 114 c 124 g 127 t 2 others
ORIGIN

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Query Match 10.6%; Score 465; DB 10; Length 481;
Best Local Similarity 100.0%; Pred. No. 8.5e-169;
Matches 465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AGGAATGACCACGGCGCCTCAGTTTCCCATTTGTATAATGGAAGCCCTGTACCAGGTGAT 60
QY 2789 tcttaagatttctctgactcagtgagctggaattcttaaatgctgtgctaggagctc 2848
Db 61 TCTTAAGATTCTCTGACTGAGTGAGTGAATTTCTAAATGCTGGTCTAGGAGCTGTC 120

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QY 2849 tccaggatggtgaggtgcttcttcggaagagagatg99gtttgagagcccaaaactg 2908
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QY 2909 ctgtcaatttgccttgcctctctgcagccctgaacttgactgaataaactccct 2968
Db 181 CTGTGCAATATGGCTTTGGCTCTTGGCAGCCCTTGAACCTTGAGTAATAACAACCTCCT 240
QY 2969 gaacctcagtttccctctctgcagaaatgggataattatgtccaggggtatatattagac 3028
Db 241 GAACCTCAGTTTCTCATCTGCAGAAATGGGATAAATATGTGCCAGGGGTATATTTAGAC 300
QY 3029 cctgtttcccttccaggggtcccccagctggtccagggcctggaaaatttctactatcc 3088
Db 301 CCTGTTCCTTTTCAGSAGGCTCCCACTGGTCCAGGGCTTGGGAAATTTCTACTTTATCC 360
QY 3089 tcattaccaggtccctctcttgcagccctgaagggtcagggtgaatcatgatggggac 3148
Db 361 TCATTACCCAGGTCCTCTTGGACCTGTAAAGGTCAGGTCAGGTGAATCAGATGGGGAC 420
QY 3149 tgagcaagtgcctgactgcagatcatgtgaaggagggactgac 3193
Db 421 TGAGCAAGTAGCTATGACTGCAGATCATGTGAAGGAAGGGACTGAC 465

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RESULT 7
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LOCUS AL449913 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
DEFINITION mRNA sequence.
ACCESSION AL449913
VERSION AL449913.1 GI:11181538
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 461)
AUTHORS Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P.
JOURNAL Unpublished (2000)
COMMENT Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquery@sanger.ac.uk
Sanger Centre name : scc3334.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="Lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue technique"

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BASE COUNT 56 a 146 c 145 g 114 t
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Best Local Similarity 100.0%; Pred. No. 7.4e-167;
Matches 460; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 336 atcaggctgctgctgcactgcagctgacttggctgaagctgctgagcggaggtt 395
Db 1 ATCAGGTCCTGCTGCTCACTGCAGCTGACTTTGGGCTAAGCTGCTGGAGCAGGAGTT 60
QY 396 cctggtggcagcctgctcctggggcctcctgcagcctcctggtggttcctcat 455
Db 61 CCTGTTGGGAGCCCTGCTCTCTGGGGGGCTCTCTCTGCTGCTGCTGCTCTCTCAT 120

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QY 456 tgactgtatggcggagcaagccatcctcctgggagcaacttggctgctgagcagcag 515
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QY 516 cctgacctgggctgctgctgctcctcctgctgctgctgctgctgctgctgctgctgct 575
Db 181 CCTGACCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 576 ctgcgcatttccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 635
Db 241 CTTCGCCATTTCCCTCTCCTCATGGTGGTGTATCTACCTGTACAGAGCTGGTGGGCC 300
QY 636 acgcacggggagctgctgctcctcctcctcctcctcctcctcctcctcctcctcctcct 695
Db 301 ACGCAGCGGGAGTGTGGTGTCCCTCTATGAGGAGGACATCACCGTGGGACATCCTGCT 360
QY 696 ctctatgcccctcaactcactgctgctgctgctgctgctgctgctgctgctgctgctgct 755
Db 361 CTCTATGCCCTCAACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 756 ctggggcactgcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 795
Db 421 CTGGGCCACTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 460

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RESULT 8
AI334230/c 454 bp mRNA EST 13-FEB-1999
LOCUS AI334230 3' mRNA sequence.
DEFINITION AI334230
ACCESSION AI334230
VERSION AI334230.1 GI:4070789
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 454)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 599 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 409.
FEATURES
Location/Qualifiers
source 1..454
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1932055"
/clone_lib="Soares_NHMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not 1;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHM, and fetal heart NbHM19w) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of 1.M.A.C.E. clones 260232-265223,
340488-345479, and 484488-489479."
BASE COUNT 128 a 112 c 97 g 117 t
ORIGIN

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ACCESSION      AL449887
VERSION        AL449887.1  GI:11181512
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 459)
AUTHORS        Stavrides,G.S., Huckle,E.J. and Deloukas,P.
TITLE          Unpublished. Stavrides,G.S., Huckle,E.J. and Deloukas,P
JOURNAL        Unpublished (2000)
COMMENT        Contact: Stavrides GS
               The Sanger Centre
               Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
               Email: humquery@sanger.ac.uk
               Sanger Centre name : sccdl338.
               Location/Qualifiers
                 1..459
                   /organism="Homo sapiens"
                   /db_xref="taxon:9606"
                   /map="20"
                   /clone_lib="Homo sapiens fetal lung (Stavrides GS)"
                   /tissue_type="Lung"
                   /dev_stage="fetal"
                   /note="cDNA fragment isolated using a cDNA end rescue
                     technique"
BASE COUNT     74 a 148 c 142 g 95 t
ORIGIN
Query Match    9.3%; Score 408; DB 10; Length 459;
Best Local Similarity 99.8%; Pred. No. 8.4e-147;
Matches 459; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 733 tgggagatggagcacatgttcgctggccactgcactgctgtcctgcaatccctcagc 792
DB 1 tggggatggagcacatgttcgctggccactgcactgctgtcctgcaatccctcagc 60
QY 793 ctctctctctctctctgctgtgacagatgagactgcaacacacagagacctatccactc 852
DB 61 CTCCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
QY 853 caggagagtgagggcccccagctggccgggggggggggggggggggggggggggggggg 912
DB 121 CAGGAGGTGAGGCGCCCAAGCTGGCGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 180
QY 913 ttcaggcacgcgataacatcgcagcgccgacccacatgggacctgggctggctgtcttc 972
DB 181 TTCAGGACGCGGATACATCGAGGCGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 240
QY 973 cagcaataacagggcgagcccaacgctgtgtgtatgctcctccacatcttcagctccgtt 1032
DB 241 CAGCAACTAACAGGCGAGCCCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 1033 gggttcacatggggatctctcagccgctgctgctctctgtgggctgtggcgcaagtgaagt 1092
DB 301 GGTTTCATGGGGGATCCTCAGCCGCTGTGCCCTCTGTGGGGCTTGGCGCAGTGAAGGTG 360
QY 1093 gcagctaccctgcagccatggggctggtagcctgcagccgagggctctgttgccta 1152
DB 361 GCAGCTACCTTGACCGGCATGGGGCTGTGTGACCGGTGCAGCGCCGCAAGGCTCTGTGCTA 420
QY 1153 gctggctgtgccctcatggccctgtccgctcagtgggcata 1191
DB 421 GCTGGCTGTGCCCTCATGGCCCTGTCCGCTCAGTGGCATA 459

RESULT 11
LOCUS      A1041537/c
DEFINITION ov82b10.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1643803
3', RNA sequence.
ACCESSION  A1041537

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VERSION        A1041537.1  GI:3280731
KEYWORDS       EST.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 532)
AUTHORS        NCI-CoAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
JOURNAL        Unpublished (1997)
COMMENT        Contact: Robert Strausberg, Ph.D.
               Email: cgapsb-femail.nih.gov
               cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Ronaldo
               , Ph.D.
               cDNA Library Arrayed by: Greg Lennon, Ph.D.
               DNA Sequencing by: Washington University Genome Sequencing Center
               Clone distribution: NCI-CGAP clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               www-bio.lnl.gov/bbrp/image/image.html
               Insert length: 1648 Std Error: 0.00
               Seq primer: -40ml3 fwd. ET from Amersham
               High quality sequence stop: 444.
               Location/Qualifiers
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                   /db_xref="taxon:9606"
                   /clone="IMAGE:1643803"
                   /clone_lib="Soares_testis_NHT"
                   /sex="male"
                   /lab_host="DH10B"
                   /note="vector: pT773D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech Laboratories
                     , Inc., and primed with a Not I - oligo(dT) primer [5',
                     TGTTACCAATCTGAGTGGGAGCGGCGGCCCAATTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT773 vector. Library
                     went through one round of normalization to Cots, and was
                     constructed by Bento Soares and M. Fatima Ronaldo."
BASE COUNT     181 a 79 c 78 g 194 t
ORIGIN
Query Match    9.2%; Score 404; DB 10; Length 532;
Best Local Similarity 99.6%; Pred. No. 2.6e-145;
Matches 504; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3837 aaaaatggagggattattcttcagtagttgaaacactgtcatccgtttcagctgacagct 3896
DB 532 AAAAAATGAGGGATTATTCTTCCAGTAGTTCACACTGTCTATCCGTTTCAGCTGACAGCT 473
QY 3897 gctcaaatcatttaagagaggtctgcacattcttcattcttcttcttcttcttcttc 3956
DB 472 GCTCAAAATCATTAAGAGGAGTCTGCATATTCATTTTTCATTTTACTTTTGTCTTCC 413
QY 3957 tcaatagtgtaacaaataatttcaaccagcttcattgcgcgaacctataccattcttcag 4016
DB 412 TCAC TAGTGTAAACAAAAATTTCAACCAGCATTCATGCCGAACCTATACCATCTCTCAG 353
QY 4017 tgcctagctgtacagttatcagggattttttattcgtagttctaaattttgtcaaaatcagtc 4076
DB 352 TGCCTAGCTGTACAGTATACAGGGATTTTATTTAGTCTTAATTTTGTCAATCATGGC 293
QY 4077 caaatcgcagtgatagttgactttggatatacaggtttggcaaaaaataataatacaaa 4136
DB 292 CAAATCGCAGTGTAGTTGACTTTGGATACAAAGGTTTGGCAAAAAATAATATTAACAA 233
QY 4137 aatattctgttaagatcaattggcttatatgatgaatttaggataaaggaattattacaataa 4196
DB 232 AATATTCTGTGAAGATCAATTTGCTATATGGAATTTAGGATAAAGATATTTACATAAA 173

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QY 4197 gaattattacaataaagaggtttattattattgtgtgtaagttgtgcaacaaacacaccctt 4256
Db 172 GAATATTACAAATAAAGAGTTTATTATTATTGTAAGTTGTGTCACAAACATACCCTT 113
QY 4257 tatctctgtaaaattatcacacacaaataaataaagaattctgtgaagaatttaattggc 4316
Db 112 TATCTCTGTAATTTATACACACAAATAATTAACAAAGATTTCTGTAAGATTAATTTGGC 53
QY 4317 tatatggaatttagtagaataattt 4342
Db 52 TATATGGAATTTAGGATAGATATT 27

RESULT 12
LOCUS BG563879 859 bp mRNA EST 10-APR-2001
DEFINITION 602584689F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4712350 5',
mRNA sequence.
ACCESSION BG563879
VERSION BG563879.1 GI:13571531
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
http://image.llnl.gov
Plate: LLCM1554 row: a column: 23
High quality sequence stop: 714.
Location/Qualifiers
1..859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4712350"
/clone_lib="NIH_MGC_76"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); site:1:
SfiI (ggcccttcggcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCGAGATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.85
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
BASE COUNT 240 a 168 c 172 g 279 t
ORIGIN

Query Match 8.7%; Score 384; DB 11; Length 859;
Best Local Similarity 99.8%; Pred. No. 9.8e-138;
Matches 504; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3179 aaggaaggactgacaaagctccagatgctgggagagaataagagctaaatagatc 3238
Db 1 AAGCAAGGACTGACAAAGAGCTCCCGAGATGCTGGGGAGAAATGAAGAGCTAAATAGATC 60

QY 3239 ctgaagtgctgagctttgtcatccatgcgtgcacatatgggtgctggcagagcccccacaa 3298
Db 61 CTAGGTGCTGATGCTTTGTTCATCCATGCTGTCACATATGGGTGCTGGCAGAGCCCCCAA 120

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QY 3299 ggactctggcctctcaggtttctctctatcttctccattctagatgcttccctgtatccag 3358
Db 121 GGACTCTGGCCTCTCGAGTTCTCTATCTTCATCTTAGAGCTTCCTCTGTATCCAG 180
QY 3359 tgaatgctggagactggcttggccaaagctgtgagagctgtgtctacattttcagatt 3418
Db 181 TGAATGCTGGAGCTGGCTTTGCCAAGCTTGTGAGAGCTGGTTGTCTACATTTTCAGGATT 240
QY 3419 tttaacaagtgtgtaaacacagcattataaaaaataaaatgatttaa-attcataatbaa 3477
Db 241 TTTACAAGTTGGTAAACACAGCCATTATATAAATAATTAATGATTATAATTAATAA 300
QY 3478 gtaaatcattataacacacacacacacacacacacacacacacacacacacacacacac 3537
Db 301 GTAAATTTACATTAACACACACACACACACACACACACACACACACACACACACACAC 360
QY 3538 ttactattatctgctcttttgaagctattttacatatagtaactcttatggagacatagg 3597
Db 361 TTACTATTATCTGTGCTTTTGGAGCTATTCTACATAGTAAGCTTTATGGAGACCTAGG 420
QY 3598 gagacacgcgcactctctctctgattcccccaactcaatcacatcatgtttagctttggtg 3657
Db 421 GAGACACGCGCATCTCTTCCTGATTCGCCACTCAATCACAATCATGTTAGTCTTTGGTGT 480
QY 3658 cttaactgctgtggggagtggtttt 3682
Db 481 CTTAACTGGCTGTGGGAGTGTTTT 505

RESULT 13
LOCUS AL449886 450 bp mRNA EST 15-NOV-2000
DEFINITION AL449886 Homo sapiens fetal lung (Stavrides GS) Homo sapiens cDNA,
mRNA sequence.
ACCESSION AL449886
VERSION AL449886.1 GI:11181511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 450)
JOURNAL Stavrides, G.S., Huckle, E.J. and Deloukas, P.
COMMENT Unpublished. Stavrides, G.S., Huckle, E.J. and Deloukas, P.
Contact: Stavrides GS
The Sanger Centre
Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK
Email: humquerry@sanger.ac.uk
Sanger Centre name: sccdl336.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20"
/clone_lib="Homo sapiens fetal lung (Stavrides GS)"
/tissue_type="lung"
/dev_stage="fetal"
/note="cDNA fragment isolated using a cDNA end rescue
technique"
BASE COUNT 75 a 148 c 133 g 94 t
ORIGIN

Query Match 8.6%; Score 378; DB 10; Length 450;
Best Local Similarity 99.8%; Pred. No. 3.1e-135;
Matches 428; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 637 cggcagcgggagtgctgtggttccctctatgagcagcagcagcagcagcagcagcagcagc 696
Db 22 CGGCAGCGGGAGTGCTGTGCTCTCTATGAGCAGGAGCATACCGTGGGCTCTCTGCTC 81
QY 697 tccatgccctcaactatgactgctggtgtaccctctgggagtgaggacatgttcggc 756

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Matches	536;	Conservative	0;	Mismatches	1;	Indels	1;	Gaps	1;
QY	3178	taagaaagggactgacaagaagctccagatgctggggagaataagaagctaaatagat	3237						
Db	1	TAAGCAAGGGACTGACAGAGAGCTCCAGATGCTGGGGAGAATGAAGAGCTTAAATAGAT	60						
QY	3238	ctaagtgctggatgctttgttcaccatgcgtgcacatagtggctgctggcagagccccc	3297						
Db	61	CCTAGGTGCTGGATGCTTTGTTCATCCATGCGTGACATATGGGTGCTGGCAGAGCCCCCA	120						
QY	3298	aggactctggcctctcgagttctcctatctctccattctccattcgtctcccttgatccca	3357						
Db	121	AGGACTCTGGGCTCTCGAGTTCTCCTATCTCTCCATCTCTAGATGCTTCCCTTGTATCCA	180						
QY	3358	gtatgtgctggagctggcttggcgaagctgtgagagctgggtgtcacattttcagat	3417						
Db	181	CTGATGTGCTGGAGCTGGCTTTGCCAAGCTTGTGAGAGCTGGTGTGTACATTTTTCAGGAT	240						
QY	3418	ttttacaagttggttaacacagagccattataaaaaattaaatgattttaa-atttataatta	3476						
Db	241	TTTTTACAAAGTTGGTAAACACACAGCCATTTATAAAAATTAATGATTTTAACATTTTATATTA	300						
QY	3477	agtaattacattataaacacaaaaattatactcaaaattcattacttaatttactacct	3536						
Db	301	AGTAAATTACATTTAAACAAAAAAATTTATACTCAAATTCATTACTTTAAATTTTACTACCT	360						
QY	3537	gttactattactgtgctttggaggctattctcacatagtaactcttatggagacctagg	3596						
Db	361	GTTACTATTATCTGTGCTTTGGGCTATTCTTACATAGTAACACTCTTATGGAGACCTAGG	420						
QY	3597	ggagacacgcgcatactctctctgattcccaactccaatgacatcatgttagtcttggtt	3656						
Db	421	GGAGACCCGCGCATCTCTTCCTGATTCGCCACTCAATGACATCATGTGTAGTCTTTGGTT	480						
QY	3657	gcttaactggctgtggggagtgcttttctgatacacaagaattagagaggactacatc	3714						
Db	481	GTTTAACTGGCTCTGGGGAGTGTTTTTGTATCACAAGATTAGAGAGACTACATC	538						

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Job time: 7337 sec